



attachment #4

## SEQUENCE LISTING

<110> BROUN, Pierre  
VAN DE LOO, Frank  
BODDUPALLI, Sekhar  
SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY  
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921  
<141> 1999-03-04

<150> 08/597,313  
<151> 1996-02-06

<150> PCT/US97/02187  
<151> 1997-02-06

<160> 15

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<213> Lesquerella fendleri

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atcatgtatgt taactgttca gttcgcttcc ggtatggccct tggatcttagc cttaacgtt 180  
tctggcagac cctacaatgg tttcgcttcc catttcttcc ccaatgttcc tatctacaaac 240  
gaccgtgaac gcctccagat ttacatcttct gatgctgttca ttcttagccgt ctgttatgg 300  
ctttaccgtt acgctgttgc acaaggacta gcctcaatgttactgtctaa cggagttccg 360  
cttttgatag ttaactttt cctcgtcttgc atcacttact tacaacacac tcaccctg 420

ttgcctcact atgattcatc agagtggat tggcttagag gagcttagc tactgttagac 480  
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cact 544

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gccacccatt ttggaccac ganccttca tttaaacacct ctctcggtct attcaccaga 240  
agagaagcca agagagagag agagagaatg ttctgaggat cattgtctc ttcatcgta 300  
ttaacgtaaag ttttttttga ccactcatat ctaaaatcta gtacatgcaa tagattaatg 360  
actgttcctt cttttgatat tttagcttc ttgaattcaa gatgggtgt ggtgaaagaa 420  
taatggttac cccctcttcc aagaatctcg aaactgaagc cctaaaacgt ggaccatgtg 480  
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aaccggataac ggaacgtggg aagaaagggtg tctactatttta caacaataag ttatggaggt 1560  
gatagggcga gagaagtgcattatcaatc ttttttttca tgtttttaggt gtcttggta 1620  
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gccttagttt gtttttttca ataatctcg agtccatnta gttgtgttct ggtgcatttt 1740  
aagaacaatgtt ttacgtgtttt aaaaactctcg gaacgaatgtt accacaanat atccaaaacc 1800  
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<212> PRT  
<213> Lesquerella fendleri

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Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys  
 85 90 95  
 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala  
 100 105 110  
 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His  
 115 120 125  
 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg  
 130 135 140  
 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 145 150 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro  
 165 170 175  
 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro  
 180 185 190  
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala  
 195 200 205  
 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu  
 210 215 220  
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 225 230 235 240  
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr  
 245 250 255  
 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe  
 260 265 270  
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp  
 275 280 285  
 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile  
 290 295 300  
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His  
 305 310 315 320  
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala  
 325 330 335  
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp  
 340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro  
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 35 40 45  
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val  
 50 55 60  
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 65 70 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe  
 85 90 95  
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly  
 100 105 110  
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu  
 115 120 125  
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 130 135 140  
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 145 150 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser  
 165 170 175  
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu  
 180 185 190  
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
 195 200 205  
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg  
 210 215 220  
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 225 230 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met  
 245 250 255

Arg	Ile	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Cys	Phe	Leu	Val	Met
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Ile	Thr	Tyr	Leu	Gln	His	Thr	His	Pro	Ala	Ile	Pro	Arg	Tyr	Gly	Ser
	275						280					285			
Ser	Glu	Trp	Asp	Trp	Leu	Arg	Gly	Ala	Met	Val	Thr	Val	Asp	Arg	Asp
	290					295				300					
Tyr	Gly	Val	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Ala	Asp	Thr	His	Val
	305					310			315			320			
Ala	His	His	Leu	Phe	Ala	Thr	Val	Pro	His	Tyr	His	Ala	Met	Glu	Ala
				325				330				335			
Thr	Lys	Ala	Ile	Lys	Pro	Ile	Met	Gly	Glu	Tyr	Tyr	Arg	Tyr	Asp	Gly
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Thr	Pro	Phe	Tyr	Lys	Ala	Leu	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Leu	Phe
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Val	Glu	Pro	Asp	Glu	Gly	Ala	Pro	Thr	Gln	Gly	Val	Phe	Trp	Tyr	Arg
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Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
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Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser
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Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
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Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
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Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe
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Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
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Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His
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 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
 165 170 175  
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
 195 200 205  
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
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 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
 225 230 235 240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr  
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 <213> Brassica napus  
  
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 35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
 65 70 75 80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
 145 150 155 160  
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly  
 165 170 175  
 Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr  
 180 185 190  
 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
 195 200 205  
 His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu  
 225 230 235 240  
 Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg  
 245 250 255  
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val  
 340 345 350  
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Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu  
35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val  
50 55 60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr  
65 70 75 80

Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser  
85 90 95

Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu  
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Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile  
115 120 125

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
130 135 140

Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr  
145 150 155 160

Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val  
165 170 175

Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro  
180 185 190

Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val  
195 200 205

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr  
210 215 220

Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr  
225 230 235 240

Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His  
245 250 255

Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr  
260 265 270

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val  
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 35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly  
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Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
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Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu  
 85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg  
 100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu  
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Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
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Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
 145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala  
 165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe  
 180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp  
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Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr  
 245 250 255  
 Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala  
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 Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly  
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 Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro  
 35 40 45  
 His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His  
 50 55 60  
 Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile  
 65 70 75 80  
 Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp  
 85 90 95  
 Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val  
 100 105 110  
 Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys  
 115 120 125  
 Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp  
 130 135 140  
 Glu Val Phe Val Pro Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro  
 145 150 155 160  
 Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln  
 165 170 175  
 Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg  
 180 185 190  
 Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr  
 195 200 205  
 Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val  
 210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
 225 230 235 240  
 Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp  
 245 250 255  
 Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His  
 260 265 270  
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met  
 275 280 285  
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp  
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 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala  
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 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr  
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 Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser  
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 Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 65 70 75 80  
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe  
 85 90 95  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro  
 100 105 110  
 Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser  
 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile  
130 135 140

Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu  
145 150 155 160

Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His  
165 170 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly  
180 185 190

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe  
195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro  
210 215 220

<210> 12

<211> 20

<212> DNA

<213> Ricinus communis

<400> 12

gctctttgt gcgctcattc

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for use as oligonucleotide primer

<400> 13

cggtaccaga aaacgccttg

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for use as oligonucleotide primer

<220>

<221> UNSURE

<222> 6, 12, 15

<223> any

<400> 14

taywsncaym gnmgncayca

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<210> 15  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: homologous regions of Ricinus communis deduced by hydroxylase sequence and Arabidopsis thaliana deduced desaturase sequence for use as oligonucleotide primer

<220>  
<221> UNSURE  
<222> 7, 10, 16  
<223> any

<400> 15  
rtgrtgngcn acrtgngtrt c

21